RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/265,606*

INPUT SET: S34472.raw

> **This Raw Listing contains the General**
> **Information Section and up to the first 5 pages.**

ENTERED

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 1                             SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5          (i) APPLICANT:     Zimmermann, Rainer; Park, John E.;
 6               Rettig, Wolfgang; Old, Lloyd J.
 7
 8          (ii) TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN
 9               ALPHA, AND USES THEREOF
10
11          (iii) NUMBER OF SEQUENCES:  10
12
13          (iv) CORRESPONDENCE ADDRESS:
14               (A) ADDRESSEE:  Felfe & Lynch
15               (B) STREET:  805 Third Avenue
16               (C) CITY:  New York City
17               (D) STATE:  New York
18               (E) COUNTRY:  USA
19               (F) ZIP:  10022
20
21          (v) COMPUTER READABLE FORM:
22               (A) MEDIUM TYPE:  Diskette, 3.5 inch, 2.0 MB  storage
23               (B) COMPUTER:  IBM PS/2
24               (C) OPERATING SYSTEM:  PC-DOS
25               (D) SOFTWARE:  Wordperfect
26
27          (vi) CURRENT APPLICATION DATA:
28               (A) APPLICATION NUMBER: 09/265,606
29               (B) FILING DATE:
30               (C) CLASSIFICATION:
31
32          (vii) PRIOR APPLICATION DATA:
33               (A) APPLICATION NUMBER:US/08/619,280
34               (B) FILING DATE:    18-MARCH-1996
35
36               (A) APPLICATION NUMBER: 08/230,491
37               (B) FILING DATE:    20-APRIL-1994
38
39          (viii) ATTORNEY/AGENT INFORMATION:
40               (A) NAME:  Hanson, Norman D.
41               (B) REGISTRATION NUMBER:  30,946
42               (C) REFERENCE/DOCKET NUMBER:  LUD 5330.1
43
44          (ix) TELECOMMUNICATION INFORMATION:
45               (A) TELEPHONE:  (212) 688-9200
46               (B) TELEFAX:  (212) 838-3884
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47      (2) INFORMATION FOR SEQ ID NO: 1:
48          (i) SEQUENCE CHARACTERISTICS:
49              (A)  LENGTH:         2815 Base pairs
50              (B)  TYPE:           nucleic acid
51              (C)  STRANDEDNESS:   double
52              (D)  TOPOLOGY:       linear
53          (xi) SEQUENCE DESCRIPTION: SEQ  ID NO: 1:
54
55

56      AAGAACGCCC CCAAAATCTG TTTCTAATTT TACAGAAATC TTTTGAAACT TGGCACGGTA   60
57      TTCAAAAGTC CGTGGAAAGA AAAAAACCTT GTCCTGGCTT CAGCTTCCAA CTACAAAGAC  120
58      AGACTTGGTC CTTTTCAACG GTTTTCACAG ATCCAGTGAC CCACGCTCTG AAGACAGAAT  180
59      TAGCTAACTT TCAAAAACAT CTGGAAAAAT GAAGACTTGG GTAAAAATCG TATTTGGAGT  240
60      TGCCACCTCT GCTGTGCTTG CCTTATTGGT GATGTGCATT GTCTTACGCC CTTCAAGAGT  300
61      TCATAACTCT GAAGAAAATA CAATGAGAGC ACTCACACTG AAGGATATTT TAAATGGAAC  360
62      ATTTTCTTAT AAAACATTTT TTCCAAACTG GATTTCAGGA CAAGAATATC TTCATCAATC  420
63      TGCAGATAAC AATATAGTAC TTTATAATAT TGAAACAGGA CAATCATATA CCATTTTGAG  480
64      TAATAGAACC ATGAAAAGTG TGAATGCTTC AAATTACGGC TTATCACCTG ATCGGCAATT  540
65      TGTATATCTA GAAAGTGATT ATTCAAAGCT TTGGAGATAC TCTTACACAG CAACATATTA  600
66      CATCTATGAC CTTAGCAATG GAGAATTTGT AAGAGGAAAT GAGCTTCCTC GTCCAATTCA  660
67      GTATTTATGC TGGTCGCCTG TTGGGAGTAA ATTAGCATAT GTCTATCAAA ACAATATCTA  720
68      TTTGAAACAA AGACCAGGAG ATCCACCTTT TCAAATAACA TTTAATGGAA GAGAAAATAA  780
69      AATATTTAAT GGAATCCCAG ACTGGGTTTA TGAAGAGGAA ATGCTTCCTA CAAAATATGC  840
70      TCTCTGGTGG TCTCCTAATG GAAAATTTTT GGCATATGCG GAATTTAATG ATAAGGATAT  900
71      ACCAGTTATT GCCTATTCCT ATTATGGCGA TGAACAATAT CCTAGAACAA TAAATATTCC  960
72      ATACCCAAAG GCTGGAGCTA AGAATCCCGT TGTTCGGATA TTTATTATCG ATACCACTTA 1020
73      CCCTGCGTAT GTAGGTCCCC AGGAAGTGCC TGTTCCAGCA ATGATAGCCT CAAGTGATTA 1080
74      TTATTTCAGT TGGCTCACGT GGGTTACTGA TGAACGAGTA TGTTTGCAGT GGCTAAAAAG 1140
75      AGTCCAGAAT GTTTCGGTCC TGTCTATATG TGACTTCAGG GAAGACTGGC AGACATGGGA 1200
76      TTGTCCAAAG ACCCAGGAGC ATATAGAAGA AAGCAGAACT GGATGGGCTG GTGGATTCTT 1260
77      TGTTTCAAGA CCAGTTTTCA GCTATGATGC CATTTCGTAC TACAAATAT TTAGTGACAA 1320
78      GGATGGCTAC AAACATATTC ACTATATCAA AGACACTGTG GAAAATGCTA TTCAAATTAC 1380
79      AAGTGGCAAG TGGGAGGCCA TAAATATATT CAGAGTAACA CAGGATTCAC TGTTTTATTC 1440
80      TAGCAATGAA TTTGAAGAAT ACCCTGGAAG AAGAAACATC TACAGAATTA GCATTGGAAG 1500
81      CTATCCTCCA AGCAAGAAGT GTGTTACTTG CCATCTAAGG AAAGAAAGGT GCCAATATTA 1560
82      CACAGCAAGT TTCAGCGACT ACGCCAAGTA CTATGCACTT GTCTGCTACG GCCCAGGCAT 1620
83      CCCCATTTCC ACCCTTCATG ATGGACGCAC TGATCAAGAA ATTAAAATCC TGGAAGAAAA 1680
84      CAAGGAATTG GAAAATGCTT TGAAAAATAT CCAGCTGCCT AAAGAGGAAA TTAAGAAACT 1740
85      TGAAGTAGAT GAAATTACTT TATGGTACAA GATGATTCTT CCTCCTCAAT TTGACAGATC 1800
86      AAAGAAGTAT CCCTTGCTAA TTCAAGTGTA TGGTGGTCCC TGCAGTCAGA GTGTAAGGTC 1860
87      TGTATTTGCT GTTAATTGGA TATCTTATCT TGCAAGTAAG GAAGGGATGG TCATTGCCTT 1920
88      GGTGGATGGT CGAGGAACAG CTTTCCAAGG TGACAAACTC CTCTATGCAG TGTATCGAAA 1980
89      GCTGGGTGTT TATGAAGTTG AAGACCAGAT TACAGCTGTC AGAAAATTCA TAGAAATGGG 2040
90      TTTCATTGAT GAAAAAAGAA TAGCCATATG GGGCTGGTCC TATGGAGGAT ACGTTTCATC 2100
91      ACTGGCCCTT GCATCTGGAA CTGGTCTTTT CAAATGTGGT ATAGCAGTGG CTCCAGTCTC 2160
92      CAGCTGGGAA TATTACGCGT CTGTCTACAC AGAGAGATTC ATGGGTCTCC CAACAAAGGA 2220
93      TGATAATCTT GAGCACTATA AGAATTCAAC TGTGATGGCA AGAGCAGAAT ATTTCAGAAA 2280
94      TGTAGACTAT CTTCTCATCC ACGGAACAGC AGATGATAAT GTGCACTTTC AAAACTCAGC 2340
95      ACAGATTGCT AAAGCTCTGG TTAATGCACA AGTGGATTTC CAGGCAATGT GGTACTCTGA 2400
96      CCAGAACCAC GGCTTATCCG GCCTGTCCAC GAACCACTTA TACACCCACA TGACCCACTT 2460
97      CCTAAAGCAG TGTTTCTCTT TGTCAGACTA AAAACGATGC AGATGCAAGC CTGTATCAGA 2520
98      ATCTGAAAAC CTTATATAAA CCCCTCAGAC AGTTTGCTTA TTTTATTTTT TATGTTGTAA 2580
99      AATGCTAGTA TAAACAAACA AATTAATGTT GTTCTAAAGG CTGTTAAAAA AAAGATGAGG 2640
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INPUT SET: S34472.raw

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100  ACTCAGAAGT TCAAGCTAAA TATTGTTTAC ATTTTCTGGT ACTCTGTGAA AGAAGAGAAA 2700
101  AGGGAGTCAT GCATTTTGCT TTGGACACAG TGTTTTATCA CCTGTTCATT TGAAGAAAAA 2760
102  TAATAAAGTC AGAAGTTCAA AAAAAAAAAA AAAAAAAAAA AAAGCGGCCG CTCGA      2815
103
104
105
106  (2)  INFORMATION FOR SEQ ID NO: 2:
107       (i)  SEQUENCE CHARACTERISTICS:
108            (A)  LENGTH:    760 amino acids
109            (B)  TYPE:      amino acid
110            (D)  TOPOLOGY: linear
111       (xi)  SEQUENCE DESCRIPTION:    SEQ ID NO: 2:
112
113
114  Met Lys Thr Trp Val Lys Ile Val Phe Gly Val Ala Thr Ser Ala Val
115                   5                  10                  15
116
117  Leu Ala Leu Leu Val Met Cys Ile Val Leu Arg Pro Ser Arg Val His
118               20                  25                  30
119
120  Asn Ser Glu Glu Asn Thr Met Arg Ala Leu Thr Leu Lys Asp Ile Leu
121           35                  40                  45
122
123  Asn Gly Thr Phe Ser Tyr Lys Thr Phe Phe Pro Asn Trp Ile Ser Gly
124       50                  55                  60
125
126  Gln Glu Tyr Leu His Gln Ser Ala Asp Asn Asn Ile Val Leu Tyr Asn
127   65                  70                  75                  80
128
129  Ile Glu Thr Gly Gln Ser Tyr Thr Ile Leu Ser Asn Arg Thr Met Lys
130                   85                  90                  95
131
132  Ser Val Asn Ala Ser Asn Tyr Gly Leu Ser Pro Asp Arg Gln Phe Val
133               100                 105                 110
134
135  Tyr Leu Glu Ser Asp Tyr Ser Lys Leu Trp Arg Tyr Ser Tyr Thr Ala
136           115                 120                 125
137
138  Thr Tyr Tyr Ile Tyr Asp Leu Ser Asn Gly Glu Phe Val Arg Gly Asn
139       130                 135                 140
140
141  Glu Leu Pro Arg Pro Ile Gln Tyr Leu Cys Trp Ser Pro Val Gly Ser
142   145                 150                 155                 160
143
144  Lys Leu Ala Tyr Val Tyr Gln Asn Asn Ile Tyr Leu Lys Gln Arg Pro
145               165                 170                 175
146
147  Gly Asp Pro Pro Phe Gln Ile Thr Phe Asn Gly Arg Glu Asn Lys Ile
148               180                 185                 190
149
150  Phe Asn Gly Ile Pro Asp Trp Val Tyr Glu Glu Glu Met Leu Pro Thr
151           195                 200                 205
152
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INPUT SET: S34472.raw

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153    Lys Tyr Ala Leu Trp Trp Ser Pro Asn Gly Lys Phe Leu Ala Tyr Ala
154        210             215             220
155
156    Glu Phe Asn Asp Lys Asp Ile Pro Val Ile Ala Tyr Ser Tyr Tyr Gly
157    225             230             235             240
158
159    Asp Glu Gln Tyr Pro Arg Thr Ile Asn Ile Pro Tyr Pro Lys Ala Gly
160                245             250             255
161
162    Ala Lys Asn Pro Val Val Arg Ile Phe Ile Ile Asp Thr Thr Tyr Pro
163                260             265             270
164
165    Ala Tyr Val Gly Pro Gln Glu Val Pro Val Pro Ala Met Ile Ala Ser
166        275             280             285
167
168    Ser Asp Tyr Tyr Phe Ser Trp Leu Thr Trp Val Thr Asp Glu Arg Val
169        290             295             300
170
171    Cys Leu Gln Trp Leu Lys Arg Val Gln Asn Val Ser Val Leu Ser Ile
172    305             310             315             320
173
174    Cys Asp Phe Arg Glu Asp Trp Gln Thr Trp Asp Cys Pro Lys Thr Gln
175                325             330             335
176
177    Glu His Ile Glu Glu Ser Arg Thr Gly Trp Ala Gly Gly Phe Phe Val
178            340             345             350
179
180    Ser Arg Pro Val Phe Ser Tyr Asp Ala Ile Ser Tyr Tyr Lys Ile Phe
181        355             360             365
182
183    Ser Asp Lys Asp Gly Tyr Lys His Ile His Tyr Ile Lys Asp Thr Val
184        370             375             380
185
186    Glu Asn Ala Ile Gln Ile Thr Ser Gly Lys Trp Glu Ala Ile Asn Ile
187    385             390             395             400
188
189    Phe Arg Val Thr Gln Asp Ser Leu Phe Tyr Ser Ser Asn Glu Phe Glu
190                405             410             415
191
192    Glu Tyr Pro Gly Arg Arg Asn Ile Tyr Arg Ile Ser Ile Gly Ser Tyr
193                420             425             430
194
195    Pro Pro Ser Lys Lys Cys Val Thr Cys His Leu Arg Lys Glu Arg Cys
196            435             440             445
197
198    Gln Tyr Tyr Thr Ala Ser Phe Ser Asp Tyr Ala Lys Tyr Tyr Ala Leu
199        450             455             460
200
201    Val Cys Tyr Gly Pro Gly Ile Pro Ile Ser Thr Leu His Asp Gly Arg
202    465             470             475             480
203
204    Thr Asp Gln Glu Ile Lys Ile Leu Glu Glu Asn Lys Glu Leu Glu Asn
205                485             490             495
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206
207  Ala Leu Lys Asn Ile Gln Leu Pro Lys Glu Glu Ile Lys Lys Leu Glu
208          500             505             510
209
210  Val Asp Glu Ile Thr Leu Trp Tyr Lys Met Ile Leu Pro Pro Gln Phe
211          515             520             525
212
213  Asp Arg Ser Lys Lys Tyr Pro Leu Leu Ile Gln Val Tyr Gly Gly Pro
214          530             535             540
215
216  Cys Ser Gln Ser Val Arg Ser Val Phe Ala Val Asn Trp Ile Ser Tyr
217  545             550             555             560
218
219  Leu Ala Ser Lys Glu Gly Met Val Ile Ala Leu Val Asp Gly Arg Gly
220          565             570             575
221  Thr Ala Phe Gln Gly Asp Lys Leu Leu Tyr Ala Val Tyr Arg Lys Leu
222          580             585             590
223
224  Gly Val Tyr Glu Val Glu Asp Gln Ile Thr Ala Val Arg Lys Phe Ile
225          595             600             605
226
227  Glu Met Gly Phe Ile Asp Glu Lys Arg Ile Ala Ile Trp Gly Trp Ser
228          610             615             620
229
230  Tyr Gly Gly Tyr Val Ser Ser Leu Ala Leu Ala Ser Gly Thr Gly Leu
231  625             630             635             640
232
233  Phe Lys Cys Gly Ile Ala Val Ala Pro Val Ser Ser Trp Glu Tyr Tyr
234          645             650             655
235
236  Ala Ser Val Tyr Thr Glu Arg Phe Met Gly Leu Pro Thr Lys Asp Asp
237          660             665             670
238
239  Asn Leu Glu His Tyr Lys Asn Ser Thr Val Met Ala Arg Ala Glu Tyr
240          675             680             685
241
242  Phe Arg Asn Val Asp Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn
243          690             695             700
244
245  Val His Phe Gln Asn Ser Ala Gln Ile Ala Lys Ala Leu Val Asn Ala
246  705             710             715             720
247
248  Gln Val Asp Phe Gln Ala Met Trp Tyr Ser Asp Gln Asn His Gly Leu
249          725             730             735
250
251  Ser Gly Leu Ser Thr Asn His Leu Tyr Thr His Met Thr His Phe Leu
252          740             745             750
253
254  Lys Gln Cys Phe Ser Leu Ser Asp
255          755             760
256
257
258
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/265,606*

INPUT SET: S34472.raw

Line	Error	Original Text